



hw-8-2.ST25.txt
SEQUENCE LISTING

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#5
JUN 19 2002
TECH CENTER 1600/2900

<110> Chandrashekhar, Ramaswamy
Morales, Tony H.

<120> PARASITIC HELMINTH CUTICLIN PROTEINS, NUCLEIC ACID MOLECULES, AND USES THEREOF

<130> HW-8-2

<140> 10/054,562

<141> 2002-01-22

<150> 09/812,642

<151> 2001-03-20

<150> 09/323,427

<151> 1999-06-01

<160> 18

<170> PatentIn version 3.1

<210> 1

<211> 1779

<212> DNA

<213> *Dirofilaria immitis*

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B1
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<213> *Dirofilaria immitis*

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atgataataa caaacgaaac tattcatggc ctaatgatga aacatttaca atatgtatgca	240
tataaaagat tactgaataa tgaataagct ttgcagaagc tataaaagcg atagaagaag	300
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ccaaatggtg acatgcagat tccattttgt actgcagcaa gtattacagg ttgtccattt	600
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hw-8-2.ST25.txt

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<213> *Dirofilaria immitis*

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<223>

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tat tcg att ccg gtt gac aat ggt gtc gaa ggt gag cca gaa att gaa 96
Tyr Ser Ile Pro Val Asp Asn Gly Val Glu Gly Glu Pro Glu Ile Glu
20 25 30

hw-8-2.ST25.txt

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gaa gga cat gtt tat gtg aaa ggt ctt tat gat caa gaa ggt tgc cgt Glu Gly His Val Tyr Val Lys Gly Leu Tyr Asp Gln Glu Gly Cys Arg 50 55 60	192
aat gat gaa ggt gga cgt caa gtt gcc gga att tca ctt cca ttt gat Asn Asp Glu Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp 65 70 75 80	240
tca tgc aat gtt gcg cgt aca cga tct ctg aat cca cgt ggt att ttt Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe 85 90 95	288
gta aca aca act gtt gtc att tcg ttt cat cca tta ttt gtt acc aaa Val Thr Thr Val Val Ile Ser Phe His Pro Leu Phe Val Thr Lys 100 105 110	336
gtt gat cgt gca tat cga gta caa tgc ttt tac atg gaa gct gat aaa Val Asp Arg Ala Tyr Arg Val Gln Cys Phe Tyr Met Glu Ala Asp Lys 115 120 125	384
aca gtt agt gca cag att gag gta tct gaa atc aca act gct ttt caa Thr Val Ser Ala Gln Ile Glu Val Ser Glu Ile Thr Thr Ala Phe Gln 130 135 140	432
act caa att gtc ccg atg cca gta tgc cgt tat gaa att ttg gat ggt Thr Gln Ile Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu Asp Gly 145 150 155 160	480
gga cca acc ggt caa cca gtt caa ttt gct atc att ggt cag cca gtt Gly Pro Thr Gly Gln Pro Val Gln Phe Ala Ile Ile Gly Gln Pro Val 165 170 175	528
tat cat aaa tgg aca tgc gat tct gaa acc gtt gat act ttc tgc gcg Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala 180 185 190	576
gtt gtc cat tcc tgc ttt gtc gat gat ggt aac ggt gat act gtc gaa Val Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Thr Val Glu 195 200 205	624
att cta aat gct gat gga tgt gct ctt gat aaa tat ttg cta aat aat Ile Leu Asn Ala Asp Gly Cys Ala Leu Asp Lys Tyr Leu Leu Asn Asn 210 215 220	672
ttg gaa tat cca aca gat tta atg gct ggc caa gaa gct cac gta tac Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His Val Tyr 225 230 235 240	720
aaa tat gcg gat cga tca cag ctt ttc tat caa tgc cag atc agt att Lys Tyr Ala Asp Arg Ser Gln Leu Phe Tyr Gln Cys Gln Ile Ser Ile 245 250 255	768
acc att aaa gaa cca aat agc gaa tgt gtt cga cca caa tgt tca gaa Thr Ile Lys Glu Pro Asn Ser Glu Cys Val Arg Pro Gln Cys Ser Glu 260 265 270	816

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gct gca gct gcg caa ctt cgt tta ctc aag aaa aga tct gca gaa ccg	912
Ala Ala Ala Gln Leu Arg Leu Leu Lys Lys Arg Ser Ala Glu Pro	
290 295 300	
gag aat atc att gat gta cga act gat atc aac acc ctt gaa att agc	960
Glu Asn Ile Ile Asp Val Arg Thr Asp Ile Asn Thr Leu Glu Ile Ser	
305 310 315 320	
gat gat aat caa gct ttg cca gtt gat tta cgt cac cgt gca ctt ctg	1008
Asp Asp Asn Gln Ala Leu Pro Val Asp Leu Arg His Arg Ala Leu Leu	
325 330 335	
caa cat aat gga caa cct gta ata ctt gct gca gta caa aat gga atc	1056
Gln His Asn Gly Gln Pro Val Ile Leu Ala Ala Val Gln Asn Gly Ile	
340 345 350	
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Cys Met Ser Pro Phe Gly Phe Ser Met Phe Met Gly Leu Ser Ile Ala	
355 360 365	
ttg att gct gcc gtc att att acc att tcg ttt aaa ttt cgt cca aat	1152
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Gln Lys Ala	
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Cys Gly Pro Thr Ser Ile Thr Ile Asn Phe Asn Thr Arg Asn Ala Phe	
35 40 45	
Glu Gly His Val Tyr Val Lys Gly Leu Tyr Asp Gln Glu Gly Cys Arg	
50 55 60	
Asn Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp	
65 70 75 80	

Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe
85 90 95

Val Thr Thr Thr Val Val Ile Ser Phe His Pro Leu Phe Val Thr Lys
100 105 110

Val Asp Arg Ala Tyr Arg Val Gln Cys Phe Tyr Met Glu Ala Asp Lys
115 120 125

Thr Val Ser Ala Gln Ile Glu Val Ser Glu Ile Thr Thr Ala Phe Gln
130 135 140

Thr Gln Ile Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu Asp Gly
145 150 155 160

Gly Pro Thr Gly Gln Pro Val Gln Phe Ala Ile Ile Gly Gln Pro Val
165 170 175

B1
Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala
180 185 190

Val Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Thr Val Glu
195 200 205

Ile Leu Asn Ala Asp Gly Cys Ala Leu Asp Lys Tyr Leu Leu Asn Asn
210 215 220

Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His Val Tyr
225 230 235 240

Lys Tyr Ala Asp Arg Ser Gln Leu Phe Tyr Gln Cys Gln Ile Ser Ile
245 250 255

Thr Ile Lys Glu Pro Asn Ser Glu Cys Val Arg Pro Gln Cys Ser Glu
260 265 270

Pro Gln Gly Phe Gly Ala Val Lys Thr Gly Gly Ala Ala Ala Lys Pro
275 280 285

Ala Ala Ala Ala Gln Leu Arg Leu Leu Lys Lys Arg Ser Ala Glu Pro
290 295 300

Glu Asn Ile Ile Asp Val Arg Thr Asp Ile Asn Thr Leu Glu Ile Ser

305

310

315

320

Asp Asp Asn Gln Ala Leu Pro Val Asp Leu Arg His Arg Ala Leu Leu
 325 330 335

Gln His Asn Gly Gln Pro Val Ile Leu Ala Ala Val Gln Asn Gly Ile
 340 345 350

Cys Met Ser Pro Phe Gly Phe Ser Met Phe Met Gly Leu Ser Ile Ala
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Gln Lys Ala
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B1
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hw-8-2.ST25.txt

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<213> *Dirofilaria immitis*

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hw-8-2.ST25.txt

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 <213> *Dirofilaria immitis*

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 gta tct gaa atg act aca gca ttc caa act caa gtg gta cca atg ccc 96
 Val Ser Glu Met Thr Ala Phe Gln Thr Gln Val Val Pro Met Pro
 20 25 30
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 Val Cys Arg Tyr Glu Ile Leu Glu Gly Pro Thr Gly Ala Pro Val
 35 40 45
 cga ttt gca atg att gga gat cat gta tat cac aaa tgg aca tgt gat 192
 Arg Phe Ala Met Ile Gly Asp His Val Tyr His Lys Trp Thr Cys Asp
 50 55 60
 tca gag act aca gat aca ttc tgt gca tta gta cat tca tgt gtt gtg 240
 Ser Glu Thr Thr Asp Thr Phe Cys Ala Leu Val His Ser Cys Val Val
 65 70 75 80
 gat gat gga aaa ggt gat gca gtg gag att ctg aat gaa gaa gga tgt 288
 Asp Asp Gly Lys Gly Asp Ala Val Glu Ile Leu Asn Glu Glu Gly Cys
 85 90 95
 gct ttg gac aaa tat tta ctc aat aat ttg gaa tat att aca gat tta 336
 Ala Leu Asp Lys Tyr Leu Leu Asn Asn Leu Glu Tyr Ile Thr Asp Leu
 100 105 110
 atg gct ggc caa gaa gct cat gtt tat aaa tat gca gat cga tca gaa 384
 Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala Asp Arg Ser Glu
 115 120 125
 ctt tac tat caa tgc cag att agt ata aca att aaa gag cca cat agc 432
 Leu Tyr Tyr Gln Cys Gln Ile Ser Ile Thr Ile Lys Glu Pro His Ser
 130 135 140
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 Glu Cys Pro Arg Pro Gln Cys Thr Glu Pro Gln Gly Phe Gly Ala Ile
 145 150 155 160
 aaa tct gga caa gga ttt gct gct gta aaa tct gct gct gca cca gct 528
 Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala
 165 170 175
 cca gaa gct tcc ttg ctt tct cca cga ttg atc aag aag cga tca att 576
 Pro Glu Ala Ser Leu Leu Ser Pro Arg Leu Ile Lys Lys Arg Ser Ile
 180 185 190

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195 200 205	
ata acc gaa gag aat ccg aac ttc tca gca aat cgt tta tca tca tca	672
Ile Thr Glu Glu Asn Pro Asn Phe Ser Ala Asn Arg Leu Ser Ser Ser	
210 215 220	
acg agc cgt gaa caa ttc aat ggt atc ttc tgt att gca tca aat gat	720
Thr Ser Arg Glu Gln Phe Asn Gly Ile Phe Cys Ile Ala Ser Asn Asp	
225 230 235 240	
att tta ctt atc att ttg ttc ggt gct atg tta gct att gct tgc ata	768
Ile Leu Leu Ile Ile Leu Phe Gly Ala Met Leu Ala Ile Ala Cys Ile	
245 250 255	
ttt ttt acc gct ttt ctt gtt cat tcc aat aat cat tct aaa tca	813
Phe Phe Thr Ala Phe Leu Val His Ser Asn Asn His Ser Lys Ser	
260 265 270	

B 1

<210> 9
<211> 271
<212> PRT
<213> *Dirofilaria immitis*
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Met Phe Leu Tyr Gly Lys Leu Ile Arg Pro Leu Val Leu Val Leu Glu
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Val Ser Glu Met Thr Thr Ala Phe Gln Thr Gln Val Val Pro Met Pro
20 25 30

Val Cys Arg Tyr Glu Ile Leu Glu Gly Gly Pro Thr Gly Ala Pro Val
35 40 45

Arg Phe Ala Met Ile Gly Asp His Val Tyr His Lys Trp Thr Cys Asp
50 55 60

Ser Glu Thr Thr Asp Thr Phe Cys Ala Leu Val His Ser Cys Val Val
65 70 75 80

Asp Asp Gly Lys Gly Asp Ala Val Glu Ile Leu Asn Glu Glu Gly Cys
85 90 95

Ala Leu Asp Lys Tyr Leu Leu Asn Asn Leu Glu Tyr Ile Thr Asp Leu
100 105 110

Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala Asp Arg Ser Glu
115 120 125

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Leu Tyr Tyr Gln Cys Gln Ile Ser Ile Thr Ile Lys Glu Pro His Ser
130 135 140

Glu Cys Pro Arg Pro Gln Cys Thr Glu Pro Gln Gly Phe Gly Ala Ile
145 150 155 160

Lys Ser Gly Gln Gly Phe Ala Ala Val Lys Ser Ala Ala Ala Pro Ala
165 170 175

Pro Glu Ala Ser Leu Leu Ser Pro Arg Leu Ile Lys Lys Arg Ser Ile
180 185 190

Asn Ser Asp Asn Thr Val Asp Val Ser Thr Gly Phe Ser Thr Val Asp
195 200 205

Ile Thr Glu Glu Asn Pro Asn Phe Ser Ala Asn Arg Leu Ser Ser Ser
210 215 220

Thr Ser Arg Glu Gln Phe Asn Gly Ile Phe Cys Ile Ala Ser Asn Asp
225 230 235 240

Ile Leu Leu Ile Ile Leu Phe Gly Ala Met Leu Ala Ile Ala Cys Ile
245 250 255

Phe Phe Thr Ala Phe Leu Val His Ser Asn Asn His Ser Lys Ser
260 265 270

<210> 10
<211> 813
<212> DNA
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attgaattgt tcacggctcg ttgatgatga taaacgattt gctgagaagt tcggattctc 180
ttcggttata tcaaccgtgc taaaaccggt actgacgtcc accgtattat cagaattaat 240
tgatcgcttc ttgatcaatc gtggagaaag caaggaagct tctggagctg gtgcagcagc 300
agattttaca gcagcaaatc cttgtccaga ttttatggca ccaaatcctt gtggctctgt 360
gcatttggt cgaggacatt cgctatgtgg ctctttaatt gttatactaa tctggcattg 420
atagtaaagt tctgatcgat ctgcataattt ataaacatga gttcttggc cagccattaa 480

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atctgtataa	tattccaaat	tattgagtaa	atatttgtcc	aaagcacatc	cttcttcatt	540
cagaatctcc	actgcac	ctttccatc	atccacaaca	catgaatgta	ctaattgcaca	600
gaatgtatct	gtagtctctg	aatcacatgt	ccatttgtga	tatacatgat	ctccaatcat	660
tgcaaatcga	acaggtgcac	cagttggtcc	accttccaaa	atctcatatc	gacatacggg	720
cattggtacc	acttgagttt	ggaatgctgt	agtcattca	gataactcaa	ggaccagttac	780
taacggtctt	atcagcttc	catataaaaa	cat			813

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B1

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<212> DNA						
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<213> Artificial sequence						
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<210> 15
 <211> 41
 <212> DNA
 <213> Artificial sequence

<220>
 <223> Synthetic Primer

<400> 15
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<210> 16
 <211> 892
 <212> DNA
 <213> Brugia malayi

<220>
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 <222> (158)...(892)
 <223>

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 ctgagaagaa atcaggaaga aagaagcaaa aagttaa atg ttg cat atg caa att 175
 Met Leu His Met Gln Ile
 1 5

tgc tca ttt ttg tca tat atg ata ata gca agt att aat gct att cca 223
 Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala Ser Ile Asn Ala Ile Pro
 10 15 20

att gat aat ggt gtc gaa agt gaa cct gaa att gaa tgt ggt cca aca 271
 Ile Asp Asn Gly Val Glu Ser Glu Pro Glu Ile Glu Cys Gly Pro Thr
 25 30 35

tca atc act gtt aat ttt aat act cga aat cct ttt gaa gga cat gta 319
 Ser Ile Thr Val Asn Phe Asn Thr Arg Asn Pro Phe Glu Gly His Val
 40 45 50

tat gct aaa gga tta tac agt aat caa gat tgt cgt agt gat gaa ggt 367
 Tyr Ala Lys Gly Leu Tyr Ser Asn Gln Asp Cys Arg Ser Asp Glu Gly
 55 60 65 70

gga cgt cag gta gcc gga ata tca tta ccg ttt gat tca tgt aat gtc 415
 Gly Arg Gln Val Ala Gly Ile Ser Leu Pro Phe Asp Ser Cys Asn Val
 75 80 85

gca cgt aca cgt tcg tta aat cca cgt gga ata ttt gtc aca gct gtt 463
 Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly Ile Phe Val Thr Ala Val
 90 95 100

gtg gta att acg ttt cat cca cag ttt atc aca aaa gtt gat cga aca 511

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Val Val Ile Thr Phe His Pro Gln Phe Ile Thr Lys Val Asp Arg Thr	105	110	115	
tat cga ttg caa tgc ttt tac atg gaa gct gat aag act gtt agc aca				559
Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala Asp Lys Thr Val Ser Thr	120	125	130	
caa att gaa gtt tcc gaa atg aca acc gta ttt gct aca caa ttg gta				607
Gln Ile Glu Val Ser Glu Met Thr Thr Val Phe Ala Thr Gln Leu Val	135	140	145	150
cca atg cct gtc ttt aga tat gag att ctg gat ggt ggt cca acc gga				655
Pro Met Pro Val Cys Arg Tyr Glu Ile Leu Asp Gly Gly Pro Thr Gly	155	160	165	
caa cct gtc cag tat gct aat att gga caa ccg gtt tat cat aaa tgg				703
Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln Pro Val Tyr His Lys Trp	170	175	180	
aca tgt gat tct gaa aca gtt gat acc ttc tgt gct ttg gta cat tcc				751
Thr Cys Asp Ser Glu Thr Val Asp Thr Phe Cys Ala Leu Val His Ser	185	190	195	
tgt ttt gtt gat gat ggc aat ggt gac agt att aat tta att aat gaa				799
Cys Phe Val Asp Asp Gly Asn Gly Asp Ser Ile Asn Leu Ile Asn Glu	200	205	210	
gaa gga tgt gca tta gat cga tat ctt cta aat aat ttg gaa tat cca				847
Glu Gly Cys Ala Leu Asp Arg Tyr Leu Leu Asn Asn Leu Glu Tyr Pro	215	220	225	230
act gat cta atg gct ggc caa gaa gct cac gta tac aaa tat gcg				892
Thr Asp Leu Met Ala Gly Gln Glu Ala His Val Tyr Lys Tyr Ala	235	240	245	
<210> 17				
<211> 245				
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<213> Brugia malayi				
<400> 17				
Met Leu His Met Gln Ile Cys Ser Phe Leu Ser Tyr Met Ile Ile Ala	1	5	10	15
Ser Ile Asn Ala Ile Pro Ile Asp Asn Gly Val Glu Ser Glu Pro Glu	20	25	30	
Ile Glu Cys Gly Pro Thr Ser Ile Thr Val Asn Phe Asn Thr Arg Asn	35	40	45	
Pro Phe Glu Gly His Val Tyr Ala Lys Gly Leu Tyr Ser Asn Gln Asp	50	55	60	

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Cys Arg Ser Asp Glu Gly Gly Arg Gln Val Ala Gly Ile Ser Leu Pro
65 70 75 80

Phe Asp Ser Cys Asn Val Ala Arg Thr Arg Ser Leu Asn Pro Arg Gly
85 90 95

Ile Phe Val Thr Ala Val Val Val Ile Thr Phe His Pro Gln Phe Ile
100 105 110

Thr Lys Val Asp Arg Thr Tyr Arg Leu Gln Cys Phe Tyr Met Glu Ala
115 120 125

Asp Lys Thr Val Ser Thr Gln Ile Glu Val Ser Glu Met Thr Thr Val
130 135 140

Phe Ala Thr Gln Leu Val Pro Met Pro Val Cys Arg Tyr Glu Ile Leu
 145 150 155 160

Asp Gly Gly Pro Thr Gly Gln Pro Val Gln Tyr Ala Asn Ile Gly Gln
165 170 175

Pro Val Tyr His Lys Trp Thr Cys Asp Ser Glu Thr Val Asp Thr Phe
180 185 190

Cys Ala Leu Val His Ser Cys Phe Val Asp Asp Gly Asn Gly Asp Ser
 195 200 205

Ile Asn Leu Ile Asn Glu Glu Gly Cys Ala Leu Asp Arg Tyr Leu Leu
210 215 220

Asn Asn Leu Glu Tyr Pro Thr Asp Leu Met Ala Gly Gln Glu Ala His
225 230 235 240

Val Tyr Lys Tyr Ala
245

<210> 18
<211> 882

<210> 18
<211> 892
<212> DNA
<213> *Brugia malayi*

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atttagaaga tatcgatcta atgcacatcc ttcttcattt attaaattaa tactgtcacc 120
attgccatca tcaacaaaac aggaatgtac caaagcacag aaggtatcaa ctgtttcaga 180
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atcacatgtc catttatgat aaaccggttg tccaatatta gcatactgga caggttgtcc 240
ggttggacca ccatccagaa tctcatatct acacacaggc attggtagca attgtgttagc 300
aaatacggtt gtcatttcgg aaacttcaat ttgtgtgcta acagtcttat cagcttccat 360
gtaaaagcat tgcaatcgat atgttcgatc aactttgtg ataaactgtg gatgaaacgt 420
aattaccaca acagctgtga caaatattcc acgtggattt aacgaacgtg tacgtgcgac 480
attacatgaa tcaaacggta atgatattcc ggctacctga cgtccacctt catcaactacg 540
acaatcttga ttactgtata atcctttagc atatacatgt cttcaaaag gatttcgagt 600
attaaaatta acagtgattt atgttggacc acattcaatt tcaggttcac tttcgacacc 660
attatcaatt ggaatagcat taatacttgc tattatcata tatgacaaaa atgagcaaatt 720
ttgcatatgc aacatttaac ttttgcttc tttcttcctg atttcttctc agtgatttagt 780
gatgaaaata gtttggaaata tagaatttagc aaaatgatta atttggaaatt gcaacaaatt 840
attgaattat tgatgatcaa ttttaatgat ctcaaacttg ggtaattaaa cc 892
